IN THE SPECIFICATION:

Please amend the specification as follows:

Please replace the section titled "RELATED APPLICATIONS" including paragraph **[0001]** with the following paragraph, which shows the changes made:

RELATED APPLICATIONS

[0001] This application is a continuation of U.S. patent application Serial No. 09/958,221, filed April 15, 2002, ~~now U.S. Patent _____, issued _____, 2003,~~ now U.S. Patent 6,686,160, issued February 3, 2004, which is a national stage of international application PCT/NL01/00177, filed March 5, 2001.

Please delete the section titled "BRIEF DESCRIPTION OF THE DRAWINGS" including paragraphs **[0016]**, **[0017]**, **[0018]**, and **[0019]** as follows:

~~BRIEF DESCRIPTION OF THE DRAWINGS~~

~~**[0016]** The samples used in the illustrations are based on high molecular weight DNA obtained from blood samples from each animal.~~

~~**[0017]** FIG. 1 illustrates the analyses of five species. Clear differences are present. Different lanes present 1) horse, 2) parrot, 3) cattle, 4) ostrich and 5) pig. The illustration shows DNA fragments ranging from sizes between 100 and 1200 bp.~~

~~**[0018]** FIG. 2 is an illustration of the analyses of five species. Clear differences are present. Different lanes present 1) horse, 2) parrot, 3) cattle, 4) ostrich and 5) pig. The illustration shows DNA fragments ranging from sizes between 250 and 300 bp.~~

~~**[0019]** FIG. 3 depicts the variation within species. Two samples of the same species (ostrich) are presented. At least three loci are presented.~~

Please replace paragraph **[0021]** with the following paragraph:

[0021] In a preferred method, genomic DNA from the sample is amplified in a first PCR at relatively low annealing temperatures. The sample may be, for example, a blood sample obtained from any one of horse, parrot, cattle, ostrich and pig, and two samples may be used to analyze at least three loci. The 5′ variation generator and the 3′ fragment generator are used to generate fragments of which a selected part is to be used in a second PCR. The first PCR is usually run under conditions under which neither the 5′ variation generator nor the 3′ fragment generator alone amplify DNA. Thus, when DNA amplification is performed using both the 5′ variation generator and the 3′ fragment generator, many resulting fragments are based on repeat sequences on one end of the genomic DNA and, at the same time, many sequences are based on an opposite end of the genomic DNA.

Please replace paragraph **[0024]** with the following paragraph:

[0024] The amplified PCR products can then be analyzed using a variety of existing methods. For instance, the analyzed products may be from about 100 to 1200 bp in length, or from about 250 to 300 bp.